Diogo M. Camacho

LEAD, PREDICTIVE BIOANALYTICS
Wyss Institute for Biologically Inspired Engineering @ Harvard University

+1 617 945 4383 | diogo.camacho@wyss.harvard.edu | diogocamacho | diogocamacho | DiogoMCamacho

Computational Systems Biology, Machine Learning, Bioinformatics

Qualifications and research interests

Highly effective computational system biologist, with graduate and post-doctoral work focusing on network inference and machine learning. Industry experience in development and implementation of computational tools for multi omics data analysis (including next-generation sequencing, metabolomics, proteomics), drug discovery, and target identification. I am interested in the application of machine learning/deep learning tools and techniques in the context of drug discovery, disease biology characterization, large data analytics for biology, while focused on bridging the gap between the computational and experimental labs through highly engaging and fruitful collaborations.

Technical Skills

Machine learning, multi omics data analytics, R/Bioconductor, keras, perl, Latex, python, MATLAB, awk, bash. Adept user of OS X/macOS, Unix. Familiarity with cloud computing architectures (AWS) and high performance computing environments.

Education

Virginia Polytechnic Institute and State University   *Blacksburg, VA*
Ph.D. in Genetics, Bioinformatics, and Computational Biology   *2007*

Faculdade de Ciencias da Universidade de Lisboa   *Lisboa, Portugal*
B. Sc. in Biochemistry   *2002*

Experience

Wyss Institute @ Harvard University   *Boston, MA*
Lead, Predictive BioAnalytics Initiative, Advanced Technology Team   *July 2016 - Present*

- Lead of the Predictive BioAnalytics Initiative at the Wyss Institute
- Development and implementation of research strategy for the Initiative, focusin on enabling ML/DL/AI capabilities
- Managerial and mentoring role, responsible for a team of computational biologists, bionformaticians, data analysts
- Involved in writing and managing federal grant applications and grant awards with DARPA, NIH
- Hands-on development of algorithms and computational approaches for dissemination internally and with corporate partners via R Shiny applications
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics, proteomics, 16S rDNA sequencing) in support of diverse grant work

Evelo Biosciences   *Cambridge, MA*
Senior Scientist, Computational Systems Biology Lead   *January 2015 - April 2016*

- Lead Computational Systems Biology efforts supporting preclinical development of microbiome-focused therapeutics for oncology
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics) as well as a 16S rDNA sequencing analysis pipeline
- Responsible for the identification of novel therapeutic opportunities based on in-house and publicly available data
- Implemented analytical software tools to be used by bench scientists in R Shiny

- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Symbiota (now Indigo Ag) *Cambridge, MA*
Consultant, Computational Systems Biology Lead *December 2014 - January 2015*

- Developed an R Shiny application for the enrichment of pathways for plant transcriptomics

Ember Therapeutics *Cambridge, MA*
Principal Scientist, Computational Systems Biology Lead *January 2014 - December 2014*

- Responsible for the identification of novel target opportunities for increased energy expenditure
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics)
- Implemented knowledge based and data driven construction of screening libraries for recombinant proteins, small peptides and RNAi
- Implemented analyses strategies (QC, statistical analyses, hit-calling) for high throughput screens
- Responsible for the implementation and maintenance of Ember⬚s portfolio management system and dissemination to senior scientific team
- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Pfizer, Inc *Cambridge, MA*
Senior Research Scientist, Computational Sciences Center of Emphasis *January 2011 - January 2014*

- Developed and implemented a network analysis tool for the characterization of differential networks in healthy and diseased populations under the scope of metabolic diseases
- Developed and implemented a methodology for metabolite set enrichment analysis for metabolomics data
- Performed data analysis in transcriptomics, proteomics and metabolomics for different partners within the organization with particular emphasis in Cardiovascular and Metabolic diseases
- Performed analysis of genetic data (genome-wide and metabolome-wide) from large sets of patient cohorts
- Implemented network inference tools for the analysis of large-scale data sets
- Involved in project decision-making process for the characterization of toxicology patterns of drugs and drug candidates

Howard Hughes Medical Institute @ Boston University *Boston, MA*
Post-doctoral Fellow *July 2007 - January 2011*

- Developed a network inference algorithm for identification of regulatory architectures of pathways
- Identified a novel mechanism of action for antifungal drugs using transcriptomics and metabolomics data
- Identified and characterized the small RNA regulatory network in bacterial systems using gene expression data
- Performed data analysis of gene expression data and metabolomics data in bacterial and fungal systems
- Consulted in the implementation and usage of inference algorithms across platforms for biotechnology/pharmaceutica companies in the Boston area

Awards and Grants

Synergistic Discovery and Design (DARPA) *$2,000,000*
co-PI *9/1/17*

Publications

- Ramesh, P, **Camacho, DM**, Collins, JJ (2019), Nu-speak: A language framework for RNA biology, *Proc. Natl. Acad. Sci. USA* (*submitted*)
- Bojar, D, **Camacho, DM**, Collins, JJ (2019), Using natural language processing to learn the language of glycans, *Nature communications* (*submitted*)
- Valeri, J, Collins, KM, Lepe, BA, Lu, TK, **Camacho, DM** (2019), A convolutional neural network for interpretable prediction and redesign of toehold switches, *Nature communications* (*submitted*)
- Jalili-Firoozinezhad, S, Gazzaniga, FS, Calamari, EL, **Camacho, DM**, Fadel, C, Nestor, B, Cronce, MJ, Tovaglieri, A, Levy, O, Gregory, KE, Breault, DT, Cabral, JMS, Kasper, DL, Novak, R, Ingber, DE (2019), A complex hu-

man gut microbiome cultured in an anaerobic intestine-on-a-chip, *Nature Biomedical Engineering*, 3, 520-531 [PubMed]

- Tovaglieri, A, Sontheimer-Phelps, A, Geirnaert, A, Prantil-Baun, R, **Camacho, DM**, Chou, DB, Jalili-Firoozinezhad, S, de Wouters, T, Kasendra, M, Super, M, Cartwright, M, Richmond, CA, Breault, DT, Lacroix, C, Ingber, DE (2019), Species-specific enhancement of enterohemorrhagic *E. coli* pathogenesis mediated by microbiome metabolites, *Microbiome*, 7, 43 [PubMed]
- **Camacho, DM**, Collins, KM, Powers, RK, Costello, JC, Collins, JJ (2018), Next-generation machine learning for biological networks, *Cell*, 173, 1581-1592 [PubMed]
- Musah, S, Dimitrakakis, N, **Camacho, DM**, Church, GM, Ingber, DE (2018), Directed differentiation of human induced pluripotent stem cells into mature kidney podocytes and establishment of a Glomerulus Chip, *Nature Protocols*, 13, 1662-1685 [PubMed]
- Paandey, SP, Winkler, JA, Li, H, **Camacho, DM**, Collins, JJ, Walker, GC (2014), Central role for RNase YbeY in Hfq-dependent and Hfq-independent small-RNA regulation in bacteria, *BMC Genomics*, 15, 121 [PubMed]
- Galagan, JE, Minch, K, Peterson, M, Lyubetskya, A, Azzizi, E, Sweet, L, Gomes, A, Rustad, T, Dolganov, G, Glotova, I, Abeel, T, Mawhinney, C, Kennedy, A, Allard, R, Brabant, W, Krueger, A, Jaini, S, Honda, B, Yu, W-H, Hickey, M, Zucker, J, Garay, C, Weiner, B, Sisk, P, Stolte, C, Winkler, J, Van de Peer, Y, Iazzetti, P, **Camacho, D**, Dreyfuss, J, Liu, Y, Dorhoi, A, Mollenkopf, H-J, Drogaris, P, Lamontagne, J, Zhou, Y, Piquenot, J, Park, ST, Raman, S, Kaufmann, S, Mohney, R, Chelsky, D, Moody, B, Sherman, D, Schoolnik, G (2013), The Mycobacterium tuberculosis regulatory network and hypoxia, *Nature*, 499, 178-183 [PubMed]
- Belenky, P, **Camacho, D**, Collins, JJ (2013), Fungicidal drugs induce a common oxidative-damage cellular death pathway, *Cell Reports*, 3, 350-358 [PubMed]
- Marbach, D, Costello, JC, Kuffner, R, Vega, N, Prill, RJ, **Camacho, DM**, Allison, KR, the DREAM5 Consortium, Kellis, M, Collins, JJ, Stolovitzky, G (2012), Wisdom of crowds for robust gene network inference, *Nature Methods*, 9, 796-804 [PubMed]
- Dwyer, DJ, **Camacho, DM**, Callura, JM, Kohanski, MA, Collins, JJ (2011), Antibiotic-induced bacterial cell death exhibits physiological and biochemical hallmarks of apoptosis, *Molecular Cell*, 46, 561-572 [PubMed]
- Modi, SR, **Camacho, DM**, Kohanski, MA, Collins, JJ (2011), Functional characterization of bacterial sRNAs using a network biology approach, *Proc. Natl. Acad. Sci. USA*, 108, 15522-15527 [PubMed]
- **Camacho, DM**, Collins, JJ (2009), Systems biology strikes gold, *Cell*, 137, 24-26 [PubMed]
- **Camacho, D**, Vera-Licona, P, Laubenbacher, R, Mendes, P (2007), Comparison of existing reverse engineering methods by use of an in silico system, *Ann. N. Y. Acad. Sci.*, 1115, 73-89 [PubMed]
- Mendes, P, **Camacho, D**, de la Fuente, A (2005), Modelling and simulation for metabolomics data analysis, *Biochem. Soc. Trans.*, 33, 1427-1429 [PubMed]
- **Camacho, D**, de la Fuente, A, Mendes, P (2005), The origin of correlations in metabolomics data, *Metabolomics*, 1, 53-63 [Link]
- Martins, AM, **Camacho, D**, Shuman, J, Sha, W, Mendes, P, Shulaev, V (2004), A systems biology study of two distinct growth phases of *Saccharomyces cerevisiae* cultures, *Curr. Genomics*, 5, 649-663 [Link]

Patents

- Soenksen, LR, **Camacho, DM**, Collins, KM, Angenent-Mari, NM, Garruss, AS, Collins, JJ, Church, GM, Method for deep learning for RNA synthetic biology (*submitted*)
- Collins, JJ, Belenky, P, **Camacho, DM** (2015), Compositions and methods for treating fungal infections, WO2014130922A1 [Link]

References

References will be provided upon request.